

REPLACEMENT FIG. 1

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1
 x_dropoff: 15 expect: 10.0 wordsize: 3 Filter:

Sequence 1 lcl|seq_1 Length 510 (1 .. 510)

Sequence 2 lcl|seq_2 Length 512 (1 .. 512)

2

NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 786 bits (2029), Expect = 0.0
 Identities = 419/522 (80%), Positives = 448/522 (85%), Gaps = 22/522 (4%)

Query: 1	MFIESFRVESPHVRYGAAEIESDYQYDTTELVHESHDGASRWIVRPKSVRYNERTTTVP	SEQ ID2
60	MFIESFRVESPHVRYGAAEIES+Y+YDTTELVHESHDGASRW+VRPKSV+Y+FRT+TTVP	
Sbjct: 1	MFIESFRVESPHVRYGAAEIESEYRYDTTELVHESHDGASRWVVRPKSVQYHFRSTTVP	SEQ ID3
60	MFIESFRVESPHVRYGAAEIESEYRYDTTELVHESHDGASRWVVRPKSVQYHFRSTTVP	
Query: 61	KLGVMLVGGNNNGSTLTAGVIANREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID2
120	KLGVMLVGGNNNGSTLTAGVIA+REGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	
Sbjct: 61	KLGVMLVGGNNNGSTLTAGVIASREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	SEQ ID3
120	KLGVMLVGGNNNGSTLTAGVIASREGISWATKDKVQQANYGSLTQASTIRVGSYNGEE	
Query: 121	IYAPFKSLLPMVNPDIVFEGGWDISNMNLADAMTRAKVLDIDLQKQLRPYME-----	SEQ ID2
173	IYAPFKSLLPMVNPDIVFEGGWDISNMNLADAMTRAKVLDIDLQKQLRPYME-----	
Sbjct: 121	IYAPFKSLLPMVNPDIVFEGGWDISNMNLADAMTRAKVLDIDLQKQLRPYMEWSCLSLAS	SEQ ID3
180	IYAPFKSLLPMVNPDIVFEGGWDISNMNLADAMTRAKVLDIDLQKQLRPYMEWSCLSLAS	
Query: 174	MVPL--PGIYDPDVIAANQGSRANNVIKGTKKEQMEQIIKDIREFKEKSVDKVVVLWTA	SEQ ID2
231	M+P + P DP A SR ++ + + KDIREFKE +K+DK VVIWTA	
Sbjct: 181	MIPTSSPLTRDP---ARTMSSRE-----PRRSRWGRSSKDIREFKENNKMDKAVVIVWTA	SEQ ID3
231	MIPTSSPLTRDP---ARTMSSRE-----PRRSRWGRSSKDIREFKENNKMDKAVVIVWTA	

Fig: 1

Query: 232 NTERYSN-VCVGLNDTHENLLASVDKNEAEISPSSTLYAIACV-MEGIIPFINGSQNTFVP SEQ ID2
 289
 NTERY+N I C I GI T ASVDI N I AEISPSSTLY I EG+ I G+ + P
 Sbjct: 232 NTERYNHCLCLGLM-TNGKPSASVDRANQAEISPSSTLYCHCLASLEGVR5ITGALKKSWP SEQ ID3
 290
 Query: 290 GLIDLAIKNCLI-GGDDFKSGQTAKMKSVLVDLVGAGIKPTSIVSYNHGNNDGMNLSA SEQ ID2
 348
 G+ DLAIK GG K G+ K K+ LVDFL+GAGIKPTSIVSYNHGNNDGMNLSA
 Sbjct: 291 GIDDLAIKKKLDPGGLIQKRGKPKKKTGLVDELMGAGIKPTSIVSYNHGNNDGTNLSA SEQ ID3
 350
 Query: 349 PQTFRSKEISKSNVVDMVSSNAILYELGEHPDHVVVIKYVPYVGDSKRAMDEYTSETFM SEQ ID2
 408
 PQTFRSKEISKSS+VVDDMVSSNAILYE GEHPDHVVVIKYVPYVGDSKRAMDEYTSETFM
 Sbjct: 351 PQTFRSKEISKSSVVDMVSSNAILYEPGEHPDHVVVIKYVPYVGDSKRAMDEYTSETFM SEQ ID3
 410
 Query: 409 GGKSTIVLHNTCEDSLLAAPIILDLVLLAELSTRIQLKAEGERKFHSFHPVATILSYLT
 468
 GGK+TIVLHNTCEDSLLAAPIILDLVLLAELSTRIQLK EGEEKFHSHFPVATILSYLT
 Sbjct: 411 GGKNTIVLHNTCEDSLLAAPIILDLVLLAELSTRIQLKGEGEEEKFHSHFPVATILSYLT
 470
 Query: 469 APLVPPGTpvvnALAKQRAMLENIMRACVGLAPENNMLEYK 510. SEQ ID2
 APLVPPGTpvvnALAKQRAMLENIMRACVGLAPENNMLEYK
 Sbjct: 471 APLVPPGTpvvnALAKQRAMLENIMRACVGLAPENNMLEYK 512 SEQ ID3
 CPU time: 0.10 user secs. 0.02 sys. secs 0.12 total
 secs.

 Gapped
 Lambda K H
 0.316 0.134 0.385

 Gapped
 Lambda K H
 0.267 0.0410 0.140

 Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 2125
 Number of Sequences: 0
 Number of extensions: 153
 Number of successful extensions: 5
 Number of sequences better than 10.0: 1
 Number of HSP's better than 10.0 without gapping: 1
 Number of HSP's successfully gapped in prelim test: 0
 Number of HSP's that attempted gapping in prelim test: 0
 Number of HSP's gapped (non-prelim): 1
 length of query: 510
 length of database: 233,319,389
 effective HSP length: 125
 effective length of query: 385
 effective length of database: 176,133,389
 effective search space: 67011354765
 effective search space used: 67011354765

Fig: 1 (Cont'd)